

Linking Archaeal Molecular Diversity and Lipid Biomarker Composition in a Hypersaline Microbial Mat Community

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Lipid biomarkers are a valuable tool for studying modern microbial ecosystems and for establishing links to the geological record. Organism source, function, and sometimes, physiological status can be established by analysis of microbial membrane lipids. Extension to pertinent microbial mat communities helps build a structural framework for contemporary microbial ecosystems, and by analogy, potential relevance to the fossilized carbon skeletons (geolipids) extracted from ancient sedimentary rock. The Mars Exploration Rovers have provided clear evidence for an early wet Mars and the presence of hypersaline evaporitic basins. Microbial communities may have evolved and flourished on an early wet Mars, if only for a brief period. On early Earth, Archean stromatolites testify to well established, photosynthetic microbial mats in hypersaline lagoonal environments often in active volcanic regions. The study of modern microbial analogs provides clues to establishing the cumulative biosignature of these early communities. Our analog system, the hypersaline benthic mats in Guerrero Negro, Baja California Sur, provide a variety of hypersaline environments associated with a spectrum of biodiversity, adaptive lifestyle, and potentially, lipid biomarkers. These cyanobacterial mats are a pertinent analog for consideration of evolutionary and microbial processes within hypersaline environments. Fluctuations in physio-chemical parameters associated with spatial and temporal scales are expressed through vast microbial metabolic diversity. A goal of our recent work has been to establish the dynamic of archaeal diversity within the highly oxic photosynthetic and adjacent anoxic layers, as it relates to methane production in this high sulfate environment, through the use of lipid biomarker and phylogenetic analyses. Membrane-associated ester-bound fatty acyl and ether-isoprenyl chains suggest the archaeal population of the upper 4 mm of the mat is small relative to bacteria (150:1), but becomes an important element of community structure in the deeper anoxic zone. Archaeal 16S rRNA and *mcrA* gene assemblages, demonstrated distinct spatial separation over the 130 mm core of at least three distinct genera within the order Methanosarcinales, as well as an abundance of uncultured members of the Thermoplasmatales and Crenarchaeota. Ether-bound lipid analysis identified abundant O-alkyl and O-isoprenyl chains throughout the core, and the presence of sn-2 hydroxyarchaeol, a biomarker for methylotrophic methanogens. A unique polar isoprenoid lipid containing a C30 chain, possibly related to the geolipid squalane, a hypersaline paleobiomarker, was most abundant within the oxic-anoxic transition zone.